

FIG. 1A

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tacacggccg cagctgaaca gcacaccgc tgtcccaagg acaaccccaa agaggggcct 60
cgactgcacc tcctcgaagt tgctggctgg ctttggcaag tgcaggaatg gtgttttgtg 120
agggcatgga tggagaagtg ccaagggccc ctgtttggtc acttccgaag agcaaaaacg 180
tgttgagagg agaccggttt aagatttcaa acagaacctc cccagcgcg c atgaaaggac 240
ttgattagca tatgtcaaga ggacccgctt atatactcgg tgtgtatgta cacaggactc 300
tgatctgac agtttgcgga attggagccc cagccaacag ccctagtcct agtattggca 360
gcggcagcta tagatatttc tgcagagcca gcagccggct cccacctacc caaggagaga 420
agatcgctcc aagacagtga gagcttcctt gccatttcag tgcaaagtcc ctccggagcg 480
acctcagagg agtaaccggg ccttaacttt ttgcgctcgt ttgctataa tttttctcta 540
tccacctcca tcccccccc acaacactct ttactggggg ggtcttttgt gttccggatc 600
tccccctcc atg gct ccc tta gcc gaa gtc ggg ggc ttt ctg ggc ggc ctg 651
      Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu
          1             5             10

gag ggc ttg ggc cag cag gtg ggt tcg cat ttc ctg ttg cct cct gcc 699
Glu Gly Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala
  15             20             25             30

ggg gag cgg ccg ccg ctg ctg ggc gag cgc agg agc gcg gcg gag cgg 747
Gly Glu Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg
          35             40             45

agc gcc cgc ggc ggg ccg ggg gct gcg cag ctg gcg cac ctg cac ggc 795
Ser Ala Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly
          50             55             60

atc ctg cgc cgc cgg cag ctc tat tgc cgc acc ggc ttc cac ctg cag 843
Ile Leu Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln
          65             70             75

atc ctg ccc gac ggc agc gtg cag ggc acc cgg cag gac cac agc ctc 891
Ile Leu Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu
          80             85             90

ttc ggt atc ttg gaa ttc atc agt gtg gca gtg gga ctg gtc agt att 939
Phe Gly Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile
          95             100             105             110

aga ggt gtg gac agt ggt ctc tat ctt gga atg aat gac aaa gga gaa 987
Arg Gly Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu
          115             120             125

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FIG. 1B

ctc tat gga tca gag aaa ctt act tcc gaa tgc atc ttt agg gag cag	1035
Leu Tyr Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln	
130 135 140	
ttt gaa gag aac tgg tat aac acc tat tca tct aac ata tat aaa cat	1083
Phe Glu Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His	
145 150 155	
gga gac act ggc cgc agg tat ttt gtg gca ctt aac aaa gac gga act	1131
Gly Asp Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr	
160 165 170	
cca aga gat ggc gcc agg tcc aag agg cat cag aaa ttt aca cat ttc	1179
Pro Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe	
175 180 185 190	
tta cct aga cca gtg gat cca gaa aga gtt cca gaa ttg tac aag gac	1227
Leu Pro Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp	
195 200 205	
cta ctg atg tac act tga agtgcgatag tgacattatg gaagagtcaa	1275
Leu Leu Met Tyr Thr	
210	
accacaacca ttctttcttg tcatagttcc catcataaaa taatgacca agcag	1330

FIG. 2

1 MAPLAEVGGFLGGLEGLGQQVGSFLLPPAGERPPLLGERRSAAERSA.R 49
| | | | | : | : . | . . | | : | | : . |
1 MAPLGEVGNVFGVQDAV..PFGNVPLPV..DSPVLLSDHLGQSEAGGLP 46

50 GGPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSLFGILE 99
| | | | | | | | | | | | | | | : | | . | . : | | | . | | | | | | |
47 RGPVAVTDLHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILE 96

100 FISVAVGLVSIRGVDSGLYLGMNDKGELYGSEKLTSECIFREQFEENWYN 149
| | : | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | |
97 FISIAGVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQECVFREQFEENWYN 146

150 TYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKRHQKFTHFLPRPVDPER 199
| | | | : | | | | | | | | | | | | | : | | . | | | | | | | | | | | | | | | | | |
147 TYSSNLYKHVDTGRRYYVALNKDGTREGTRTKRHQKFTHFLPRPVDPAK 196

200 VPELYKDLLMYT 211
| | | | | : | | .
197 VPELYKDILSQS 208

FIG. 3

1 MAPLAEVGGFLGGLEGLGQQVGSFHLLPPAGERPPLLGERSSAAERSA.R 49
||| ||| : | : . |. .|| : || : .|
1 MAPLGEVGSYFGVQDAV..PFGNVPVLPV..DSPVLLSDHLGQSEAGGLP 46

50 GGPGAAQLAHLHGILRRRQLYCRTGFHLQILPDGSVQGTRQDHSFLFGILE 99
|| | || ||||| ||||| :| |.|. : |||. ||| |||||
47 RGPVTDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILE 96

100 FISVAVGLVSIRGVDSGLYLG MNDKGELYGSEKLTSECIFREQFEENWYN 149
||| : ||||| ||||| ||||| : ||||| ||||| ||| : ||||| |||||
97 FISIAVGLVSIRGVDSGLYLG MNEKGELYGSEKLTQECVFEENWYN 146

150 TYSSNIYKHGDTGRRYFVALNKDGT PRDGARSKRHQKFTHFLPRPVDPER 199
||| : ||| ||||| : ||||| ||||| : | |. ||||| ||||| ||||| : :
147 TYSSNLYKHVDTGRRYYVALNKDGT PREGTRTKRHQKFTHFLPRPVD PDK 196

200 VPELYKD LLMYT 211
||| ||| : | .
197 VPELYKDILSQS 208

FIG. 4

hu	FGF-9	MAPLGEVGNV	FGVQDAV..P	FGNVPVLPV.	.DSPVLLSDH	LQQSEAGGLP	RGPAVTDLDH
hu	FGF-16	MA...EVGV	FASLDWDLHG	FSSSLGNVPL	ADSPGFLNER	LQIE.GKLQ	RGSP.TDFAH
hu	FGF-L	MAPLAEVGGF	LGGLEGLGQQ	VGSHFLLPPA	GERPPLLGER	RSAAERSA.R	GGPGAAQLAH
mu	FGF-9	MAPLGEVGSY	FGVQDAV..P	FGNVPVLPV.	.DSPVLLNDH	LQQSEAGGLP	RGPAVTDLDH
ra	FGF-16	MA...EVGV	FASLDWDLQG	FSSSLGNVPL	ADSPGFLNER	LQIE.GKLQ	RGSP.TDFAH
hu	FGF-9	LKGILRRRQL	YCRTGFHLEI	FPNGTIQGTR	KHSRFGILE	FISIAVGLVS	IRGVDSGLYL
hu	FGF-16	LKGILRRRQL	YCRTGFHLEI	FPNGTVHGTR	HDHSRFGILE	FISLAVGLIS	IRGVDSGLYL
hu	FGF-L	LHGILRRRQL	YCRTGFHLQI	LPDGSVQGTR	QDHSLFGILE	FISVAVGLVS	IRGVDSGLYL
mu	FGF-9	LKGILRRRQL	YCRTGFHLEI	FPNGTIQGTR	KHSRFGILE	FISIAVGLVS	IRGVDSGLYL
ra	FGF-16	LKGILRRRQL	YCRTGFHLEI	FPNGTVHGTR	HDHSRFGILE	FISLAVGLIS	IRGVDSGLYL
hu	FGF-9	GMNEKGELYG	SEKLTQECVF	REQFEENWYN	TYSSNLYKHV	DTGRRYYVAL	NKDGTPREGT
hu	FGF-16	GMNERGELYG	SKKLTRECVF	REQFEENWYN	TYASTLYKHS	DSERQYYVAL	NKDGSPREGY
hu	FGF-L	GMNDKGELYG	SEKLTSECIF	REQFEENWYN	TYSSNIYKHG	DTGRRYFVAL	NKDGTPRDGA
mu	FGF-9	GMNEKGELYG	SEKLTQECVF	REQFEENWYN	TYSSNLYKHV	DTGRRYYVAL	NKDGTPREGT
ra	FGF-16	GMNERGELFG	SKKLTRECVF	REQFEENWYN	TYASTLYKHS	DSERQYYVAL	NKDGSPREGY
hu	FGF-9	RTKRHQKFTH	FLPRPVDPDK	VPELYKDILS	QS		
hu	FGF-16	RTKRHQKFTH	FLPRPVDPDK	LPSMSRDLFH	YR		
hu	FGF-L	RSKRHQKFTH	FLPRPVDPER	VPELYKDILLM	YT		
mu	FGF-9	RTKRHQKFTH	FLPRPVDPDK	VPELYKDILS	QS		
ra	FGF-16	RTKRHQKFTH	FLPRPVDPDK	LPSMSRDLFR	YR		